

We claim:

1. A substantially purified nucleic acid molecule comprising a nucleic acid sequence wherein the nucleic acid sequence:

- 5 i) hybridizes under stringent conditions with a sequence selected from the group consisting of SEQ ID NO:1 through 57,467, and the complements thereof; or
- ii) exhibits an 85% or greater identity to a sequence selected from the group consisting of SEQ ID NO:1 through 57,467.

10 2. The nucleic acid molecule of claim 1, wherein the nucleic acid sequence exhibits a 90% or greater identity to a nucleic acid sequence selected from the group consisting of SEQ ID NO:1 through 57,467.

15 3. The nucleic acid molecule of claim 1, wherein the nucleic acid sequence exhibits a 95% or greater identity to a nucleic acid sequence selected from the group consisting of SEQ ID NO:1 through 57,467.

20 4. The nucleic acid molecule of claim 1, wherein the nucleic acid sequence exhibits a 99% or greater identity to a nucleic acid sequence selected from the group consisting of SEQ ID NO:1 through 57,467.

 5. The nucleic acid molecule of claim 1, wherein the nucleic acid sequence comprises a sequence selected from the group consisting of SEQ ID NO:1 through

57,467.

6. The nucleic acid molecule of claim 1, wherein the nucleic acid molecule is operably linked to a heterologous structural nucleic acid sequence.

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7. The nucleic acid molecule of claim 6, wherein the structural nucleic acid sequence encodes a protein selected from the group consisting of a yield protein, a stress resistance protein, a developmental control protein, a tissue differentiation protein, a meristem protein, an environmentally responsive protein, a senescence protein, a hormone responsive protein, an abscission protein, a source protein, a sink protein, a flower control protein, a seed protein, an herbicide resistance protein, a disease resistance protein, a fatty acid biosynthetic enzyme, a tocopherol biosynthetic enzyme, an amino acid biosynthetic enzyme, and an insecticidal protein.

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8. The nucleic acid molecule of claim 1, wherein the nucleic acid molecule further comprises one or more cis-acting nucleic acid elements.

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9. The nucleic acid molecule of claim 1, wherein the nucleic acid molecule further comprises a 5' leader sequence selected from the group consisting of dSSU 5', PetHSP70 5', and GmHSP17.9 5'.

10. The nucleic acid molecule of claim 1, wherein the nucleic acid molecule further comprises a 3' untranslated region.

11. The nucleic acid molecule of claim 10, wherein the 3' untranslated region is selected from the group consisting of NOS 3', E9 3', ADR12 3', 7S α 3', 11S 3', and albumin 3'.

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12. The nucleic acid molecule of claim 1, wherein the nucleic acid molecule further comprises an intron that is heterologous with respect to the structural nucleic acid sequence.

10 13. The nucleic acid molecule of claim 12, wherein the intron is selected from the group consisting of the rice actin intron and the corn HSP70 intron.

14. The nucleic acid molecule of claim 6, wherein the nucleic acid molecule expresses the structural nucleic acid sequence in an amount greater than 0.5% (w/w) of
15 the total mRNA.

15. The nucleic acid molecule of claim 6, wherein the nucleic acid molecule expresses the structural nucleic acid sequence in an amount greater than 1% (w/w) of the total mRNA.

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16. The nucleic acid molecule of claim 6, wherein the nucleic acid molecule expresses the structural nucleic acid sequence in an amount greater than 2% (w/w) of the

total mRNA.

17. The nucleic acid molecule of claim 1, wherein said substantially purified nucleic acid molecule is operably linked to a heterologous nucleic acid molecule and said
5 heterologous nucleic acid molecule codes for an mRNA that is complementary to an mRNA that is present in a cell.

18. A transgenic plant containing a nucleic acid molecule that comprises in the 5' to 3' direction:

10 a nucleic acid sequence that:

i) hybridizes under stringent conditions with a sequence selected from the group consisting of SEQ ID NO:1 through 57,467, and the complements thereof; or

ii) exhibits an 85% or greater identity to a sequence selected from the group consisting of SEQ ID NO:1 through 57,467;

15 operably linked to a structural nucleic acid sequence;

wherein the nucleic acid sequence is heterologous with respect to the structural nucleic acid sequence.

19. The transgenic plant of claim 18, wherein the nucleic acid sequence is
20 90% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NO:1 through 57,467.

20. The transgenic plant of claim 18, wherein the nucleic acid sequence is

95% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NO:1 through 57,467.

21. The transgenic plant of claim 18, wherein the nucleic acid sequence is
5 99% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NO:1 through 57,467.

22. The transgenic plant of claim 18, wherein the nucleic acid sequence
comprises a nucleic acid sequence selected from the group consisting of SEQ ID NO:1
10 through 57,467.

23. The transgenic plant of claim 18, wherein the structural nucleic acid
sequence encodes a protein selected from the group consisting of a yield protein, a stress
resistance protein, a developmental control protein, a tissue differentiation protein, a
15 meristem protein, an environmentally responsive protein, a senescence protein, a
hormone responsive protein, an abscission protein, a source protein, a sink protein, a
flower control protein, a seed protein, an herbicide resistance protein, a disease resistance
protein, a fatty acid biosynthetic enzyme, a tocopherol biosynthetic enzyme, an amino
acid biosynthetic enzyme, and an insecticidal protein.

24. The transgenic plant of claim 18, wherein the nucleic acid molecule
further comprises one or more cis-acting nucleic acid elements.

25. The transgenic plant of claim 18, wherein the nucleic acid molecule further comprises a 5' leader sequence selected from the group consisting of dSSU 5', PetHSP70 5', and GmHSP17.9 5'.

5 26. The transgenic plant of claim 18, wherein the nucleic acid molecule further comprises a 3' untranslated region.

27. The transgenic plant of claim 26, wherein the 3' untranslated region is selected from the group consisting of NOS 3', E9 3', ADR12 3', 7S α 3', 11S 3', and
10 albumin 3'.

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27. The transgenic plant of claim 18, wherein the nucleic acid molecule further comprises an intron that is heterologous with respect to the structural nucleic acid sequence.

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28. The transgenic plant of claim 28, wherein the intron is selected from the group consisting of the rice actin intron and the corn HSP70 intron.

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29. The transgenic plant of claim 18, wherein the plant is rice, sorghum,
20 maize, barley, or wheat.

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30. The transgenic plant of claim 18, wherein the promoter expresses the

structural nucleic acid sequence in an amount greater than 0.5% (w/w) of the total cellular RNA or protein.

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~~31~~. The transgenic plant of claim 18, wherein the promoter expresses the
5 structural nucleic acid sequence in an amount greater than 1% (w/w) of the total cellular RNA or protein.

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~~32~~. The transgenic plant of claim 18, wherein the promoter expresses the
10 structural nucleic acid sequence in an amount greater than 2% (w/w) of the total cellular RNA or protein.

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~~33~~. The transgenic plant of claim 18, wherein said nucleic acid molecule is
operably linked to a heterologous nucleic acid molecule and said heterologous nucleic
acid molecule encodes an mRNA that is complementary to an mRNA that is present in
15 said transgenic plant.

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~~34~~. A seed from the transgenic plant of claim 18.

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~~35~~. A fertile transgenic plant from the seed of claim 18.

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~~36~~. A method of transforming a host cell comprising:

a) providing a nucleic acid molecule that comprises in the 5' to 3' direction:
a nucleic acid sequence that:

i) hybridizes under stringent conditions with a sequence selected from the group consisting of SEQ ID NO:1 through 57,467, and the complements thereof; or

ii) exhibits an 85% or greater identity to a sequence selected from the group consisting of SEQ ID NO:1 through 57,467;

5 operably linked to a structural nucleic acid sequence; and

b) transforming said plant with the nucleic acid molecule.

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